SEQUENCE LISTING

<110> Fox, Brian A.
     Gao, Zeren
     Shoemaker, Kimberly E.

<120> NEUROPILIN HOMOLOG ZCUB5

<130> 00-62

<150> US 60/249,004
<151> 2000-11-15

<160> 19

<170> FastSEQ for Windows Version 3.0

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<212> DNA
<213> Homo sapiens

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<221> CDS
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               Met Val Pro Gly Ala Arg Gly Gly Gly Ala Leu Ala
                1               5                   10

cgg gct gcc ggg cgg ggc ctc ctg gct ttg ctg ctc gcg gtc tcc gcc     159
Arg Ala Ala Gly Arg Gly Leu Leu Ala Leu Leu Leu Ala Val Ser Ala
         15                  20                  25

ccg ctc cgg ctg cag gcg gag gag ctg ggt gat ggc tgt gga cac cta     207
Pro Leu Arg Leu Gln Ala Glu Glu Leu Gly Asp Gly Cys Gly His Leu
      30                  35                  40
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gtg act tat cag gat agt ggc aca atg aca tct aag aat tat ccc ggg      255
Val Thr Tyr Gln Asp Ser Gly Thr Met Thr Ser Lys Asn Tyr Pro Gly
45              50                  55                  60


acc tac ccc aat cac act gtt tgc gaa aag aca att aca gta cca aag      303
Thr Tyr Pro Asn His Thr Val Cys Glu Lys Thr Ile Thr Val Pro Lys
                 65                  70                  75


ggg aaa aga ctg att ctg agg ttg gga gat ttg gat atc gaa tcc cag      351
Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu Asp Ile Glu Ser Gln
             80                  85                  90


acc tgt gct tct gac tat ctt ctc ttc acc agc tct tca gat caa tat      399
Thr Cys Ala Ser Asp Tyr Leu Leu Phe Thr Ser Ser Ser Asp Gln Tyr
             95                  100                 105


ggt cca tac tgt gga agt atg act gtt ccc aaa gaa ctc ttg ttg aac      447
Gly Pro Tyr Cys Gly Ser Met Thr Val Pro Lys Glu Leu Leu Leu Asn
        110                 115                 120


aca agt gaa gta acc gtc cgc ttt gag agt gga tcc cac att tct ggc      495
Thr Ser Glu Val Thr Val Arg Phe Glu Ser Gly Ser His Ile Ser Gly
125                 130                 135                 140


cgg ggt ttt ttg ctg acc tat gcg agc agc gac cat cca gat tta ata      543
Arg Gly Phe Leu Leu Thr Tyr Ala Ser Ser Asp His Pro Asp Leu Ile
                 145                 150                 155


aca tgt ttg gaa cga gct agc cat tat ttg aag aca gaa tac agc aaa      591
Thr Cys Leu Glu Arg Ala Ser His Tyr Leu Lys Thr Glu Tyr Ser Lys
             160                 165                 170


ttc tgc cca gct ggt tgt aga gac gta gca gga gac att tct ggg aat      639
Phe Cys Pro Ala Gly Cys Arg Asp Val Ala Gly Asp Ile Ser Gly Asn
        175                 180                 185


atg gta gat gga tat aga gat acc tct tta ttg tgc aaa gct gcc atc      687
Met Val Asp Gly Tyr Arg Asp Thr Ser Leu Leu Cys Lys Ala Ala Ile
        190                 195                 200


cat gca gga ata att gct gat gaa cta ggt ggc cag atc agt gtg ctt      735
His Ala Gly Ile Ile Ala Asp Glu Leu Gly Gly Gln Ile Ser Val Leu
205                 210                 215                 220
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cag cgc aaa ggg atc agt cga tat gaa ggg att ctg gcc aat ggt gtt       783
Gln Arg Lys Gly Ile Ser Arg Tyr Glu Gly Ile Leu Ala Asn Gly Val
            225             230             235

ctt tcg agg gat ggt tcc ctg tca gac aag cga ttt ctg ttt acc tcc       831
Leu Ser Arg Asp Gly Ser Leu Ser Asp Lys Arg Phe Leu Phe Thr Ser
            240             245             250

aat ggt tgc agc aga tcc ttg agt ttt gaa cct gac ggg caa atc aga       879
Asn Gly Cys Ser Arg Ser Leu Ser Phe Glu Pro Asp Gly Gln Ile Arg
            255             260             265

gct tct tcc tca tgg cag tcg gtc aat gag agt gga gac caa gtt cac       927
Ala Ser Ser Ser Trp Gln Ser Val Asn Glu Ser Gly Asp Gln Val His
        270             275             280

tgg tct cct ggc caa gcc cga ctt cag gac caa ggc cca tca tgg gct       975
Trp Ser Pro Gly Gln Ala Arg Leu Gln Asp Gln Gly Pro Ser Trp Ala
285             290             295             300

tcg ggc gac agt agc aac aac cac aaa cca cga gag tgg ctg gag atc      1023
Ser Gly Asp Ser Ser Asn Asn His Lys Pro Arg Glu Trp Leu Glu Ile
            305             310             315

gat ttg ggg gag aaa aag aaa ata aca gga att agg acc aca gga tct      1071
Asp Leu Gly Glu Lys Lys Lys Ile Thr Gly Ile Arg Thr Thr Gly Ser
            320             325             330

aca cag tcg aac ttc aac ttt tat gtt aag agt ttt gtg atg aac ttc      1119
Thr Gln Ser Asn Phe Asn Phe Tyr Val Lys Ser Phe Val Met Asn Phe
            335             340             345

aaa aac aat aat tct aag tgg aag acc tat aaa gga att gtg aat aat      1167
Lys Asn Asn Asn Ser Lys Trp Lys Thr Tyr Lys Gly Ile Val Asn Asn
            350             355             360

gaa gaa aag gtg ttt cag ggt aac tct aac ttt cgg gac cca gtg caa      1215
Glu Glu Lys Val Phe Gln Gly Asn Ser Asn Phe Arg Asp Pro Val Gln
365             370             375             380
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aac aat ttc atc cct ccc atc gtg gcc aga tat gtg cgg gtt gtc ccc          1263
Asn Asn Phe Ile Pro Pro Ile Val Ala Arg Tyr Val Arg Val Val Pro
                385                    390                395

cag aca tgg cac cag agg ata gcc ttg aag gtg gag ctc att ggt tgc          1311
Gln Thr Trp His Gln Arg Ile Ala Leu Lys Val Glu Leu Ile Gly Cys
                400                    405                410

cag att aca caa ggt aat gat tca ttg gtg tgg cgc aag aca agt caa          1359
Gln Ile Thr Gln Gly Asn Asp Ser Leu Val Trp Arg Lys Thr Ser Gln
                415                    420                425

agc acc agt gtt tca act aag aaa gaa gat gag aca atc aca agg ccc          1407
Ser Thr Ser Val Ser Thr Lys Lys Glu Asp Glu Thr Ile Thr Arg Pro
                430                    435                440

atc ccc tcg gaa gaa aca tcc aca gga ata aac att aca acg gtg gct          1455
Ile Pro Ser Glu Glu Thr Ser Thr Gly Ile Asn Ile Thr Thr Val Ala
445                    450                    455                460

att cca ttg gtg ctc ctt gtt gtc ctg gtg ttt gct gga atg ggg atc          1503
Ile Pro Leu Val Leu Leu Val Val Leu Val Phe Ala Gly Met Gly Ile
                465                    470                475

ttt gca gcc ttt aga aag aag aag aag aaa gga agt ccg tat gga tca          1551
Phe Ala Ala Phe Arg Lys Lys Lys Lys Lys Gly Ser Pro Tyr Gly Ser
                480                    485                490

gca gag gct cag aaa aca gac tgt tgg aag cag att aaa tat ccc ttt          1599
Ala Glu Ala Gln Lys Thr Asp Cys Trp Lys Gln Ile Lys Tyr Pro Phe
                495                    500                505

gcc aga cat cag tca gct gag ttt acc atc agc tat gat aat gag aag          1647
Ala Arg His Gln Ser Ala Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys
                510                    515                520

gag atg aca caa aag tta gat ctc atc aca agt gat atg gca gat tac          1695
Glu Met Thr Gln Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr
525                    530                    535                540

cag cag ccc ctc atg att ggc acc ggg aca gtc acg agg aag ggc tcc          1743
Gln Gln Pro Leu Met Ile Gly Thr Gly Thr Val Thr Arg Lys Gly Ser
                545                    550                555
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acc ttc cgg ccc atg gac acg gat gcc gag gag gca ggg gtg agc acc      1791
Thr Phe Arg Pro Met Asp Thr Asp Ala Glu Glu Ala Gly Val Ser Thr
        560             565                 570

gat gcc ggc ggc cac tat gac tgc ccg cag cgg gcc ggc cgc cac gag      1839
Asp Ala Gly Gly His Tyr Asp Cys Pro Gln Arg Ala Gly Arg His Glu
        575             580                 585

tac gcg ctg ccc ctg gcg ccc ccg gag ccc gag tac gcc acg ccc atc      1887
Tyr Ala Leu Pro Leu Ala Pro Pro Glu Pro Glu Tyr Ala Thr Pro Ile
        590             595                 600

gtg gag cgg cac gtg ctg cgc gcc cac acg ttc tct gcg cag agc ggc      1935
Val Glu Arg His Val Leu Arg Ala His Thr Phe Ser Ala Gln Ser Gly
605             610                 615                 620

tac cgc gtc cca ggg ccc cag ccc ggc cac aaa cac tcc ctc tcc tcg      1983
Tyr Arg Val Pro Gly Pro Gln Pro Gly His Lys His Ser Leu Ser Ser
            625             630                 635

ggc ggc ttc tcc ccc gta gcg ggt gtg ggc gcc cag gac gga gac tat      2031
Gly Gly Phe Ser Pro Val Ala Gly Val Gly Ala Gln Asp Gly Asp Tyr
            640             645                 650

caa agg cca cac agc gca cag cct gcg gac agg ggc tac gac cgg ccc      2079
Gln Arg Pro His Ser Ala Gln Pro Ala Asp Arg Gly Tyr Asp Arg Pro
            655             660                 665

aaa gct gtc agc gcc ctc gcc acc gaa agc gga cac cct gac tct cag      2127
Lys Ala Val Ser Ala Leu Ala Thr Glu Ser Gly His Pro Asp Ser Gln
        670             675                 680

aag ccc cca acg cat ccc ggg acg agt gac agc tat tct gcc ccc aga      2175
Lys Pro Pro Thr His Pro Gly Thr Ser Asp Ser Tyr Ser Ala Pro Arg
685             690                 695                 700

gac tgc ctc aca ccc ctc aac cag acg gcc atg act gcc ctt ttg tga      2223
Asp Cys Leu Thr Pro Leu Asn Gln Thr Ala Met Thr Ala Leu Leu  *
            705             710                 715

acacaatgtg aaagaagcct gctgtggtac tgagcgtcgg gctgtcacaa ggcactggaa   2283
gaagggagcc tgctggtcca gagtgtgcgt gtgtatcgaa ctgaaagcat ttttaacatt   2343
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cttctcctgg aagaaatgaa ttacttgaag catgaaaagc acaccagggt ggttgtttat    2403
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gtttccttag tctccacttc agagggggat gcgaagaggt cggcccagct ccggtgacca    2523
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taaaaatatt gctgaggtca gacgccacaa ttttcatgac tttcttcaga agtagcacat    2643
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tcattttata agaaatgatt ttcccctcaa ggaggcgtct gtaattccag aacagtccag    2823
acatcagctg tacctcatgc tcagtagttt ttatttgagt ttcttttgtg agttaactat    2883
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ggaccaaaaa ttttttttccc tgaagaatgt attataaccc tatttgtgtg gttattacat    3003
cctgtgaaat gtatatatgt taaaataatg ggggtgctgg aaggtcatgg cagactagct    3063
gctggttagt gtggagggga agtggtttac tttgtagagt ttacatggtt ttatgcgcac    3123
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<212> PRT
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            20                  25                  30
Gln Ala Glu Glu Leu Gly Asp Gly Cys Gly His Leu Val Thr Tyr Gln
        35                  40                  45
Asp Ser Gly Thr Met Thr Ser Lys Asn Tyr Pro Gly Thr Tyr Pro Asn
    50                  55                  60
His Thr Val Cys Glu Lys Thr Ile Thr Val Pro Lys Gly Lys Arg Leu
65                  70                  75                  80
Ile Leu Arg Leu Gly Asp Leu Asp Ile Glu Ser Gln Thr Cys Ala Ser
                85                  90                  95
Asp Tyr Leu Leu Phe Thr Ser Ser Asp Gln Tyr Gly Pro Tyr Cys
            100                 105                 110
Gly Ser Met Thr Val Pro Lys Glu Leu Leu Leu Asn Thr Ser Glu Val
            115                 120                 125
Thr Val Arg Phe Glu Ser Gly Ser His Ile Ser Gly Arg Gly Phe Leu
    130                 135                 140
Leu Thr Tyr Ala Ser Ser Asp His Pro Asp Leu Ile Thr Cys Leu Glu
145                 150                 155                 160
Arg Ala Ser His Tyr Leu Lys Thr Glu Tyr Ser Lys Phe Cys Pro Ala
                165                 170                 175
```

```
Gly Cys Arg Asp Val Ala Gly Asp Ile Ser Gly Asn Met Val Asp Gly
        180                 185                 190
Tyr Arg Asp Thr Ser Leu Leu Cys Lys Ala Ala Ile His Ala Gly Ile
        195                 200                 205
Ile Ala Asp Glu Leu Gly Gly Gln Ile Ser Val Leu Gln Arg Lys Gly
    210                 215                 220
Ile Ser Arg Tyr Glu Gly Ile Leu Ala Asn Gly Val Leu Ser Arg Asp
225                 230                 235                 240
Gly Ser Leu Ser Asp Lys Arg Phe Leu Phe Thr Ser Asn Gly Cys Ser
                245                 250                 255
Arg Ser Leu Ser Phe Glu Pro Asp Gly Gln Ile Arg Ala Ser Ser Ser
                260                 265                 270
Trp Gln Ser Val Asn Glu Ser Gly Asp Gln Val His Trp Ser Pro Gly
        275                 280                 285
Gln Ala Arg Leu Gln Asp Gln Gly Pro Ser Trp Ala Ser Gly Asp Ser
    290                 295                 300
Ser Asn Asn His Lys Pro Arg Glu Trp Leu Glu Ile Asp Leu Gly Glu
305                 310                 315                 320
Lys Lys Lys Ile Thr Gly Ile Arg Thr Thr Gly Ser Thr Gln Ser Asn
                325                 330                 335
Phe Asn Phe Tyr Val Lys Ser Phe Val Met Asn Phe Lys Asn Asn Asn
                340                 345                 350
Ser Lys Trp Lys Thr Tyr Lys Gly Ile Val Asn Asn Glu Glu Lys Val
        355                 360                 365
Phe Gln Gly Asn Ser Asn Phe Arg Asp Pro Val Gln Asn Asn Phe Ile
    370                 375                 380
Pro Pro Ile Val Ala Arg Tyr Val Arg Val Val Pro Gln Thr Trp His
385                 390                 395                 400
Gln Arg Ile Ala Leu Lys Val Glu Leu Ile Gly Cys Gln Ile Thr Gln
                405                 410                 415
Gly Asn Asp Ser Leu Val Trp Arg Lys Thr Ser Gln Ser Thr Ser Val
                420                 425                 430
Ser Thr Lys Lys Glu Asp Glu Thr Ile Thr Arg Pro Ile Pro Ser Glu
        435                 440                 445
Glu Thr Ser Thr Gly Ile Asn Ile Thr Thr Val Ala Ile Pro Leu Val
    450                 455                 460
Leu Leu Val Val Leu Val Phe Ala Gly Met Gly Ile Phe Ala Ala Phe
465                 470                 475                 480
Arg Lys Lys Lys Lys Lys Gly Ser Pro Tyr Gly Ser Ala Glu Ala Gln
                485                 490                 495
Lys Thr Asp Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg His Gln
        500                 505                 510
```

```
Ser Ala Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu Met Thr Gln
        515                 520                 525
Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr Gln Gln Pro Leu
    530                 535                 540
Met Ile Gly Thr Gly Thr Val Thr Arg Lys Gly Ser Thr Phe Arg Pro
545                 550                 555                 560
Met Asp Thr Asp Ala Glu Glu Ala Gly Val Ser Thr Asp Ala Gly Gly
                565                 570                 575
His Tyr Asp Cys Pro Gln Arg Ala Gly Arg His Glu Tyr Ala Leu Pro
            580                 585                 590
Leu Ala Pro Pro Glu Pro Glu Tyr Ala Thr Pro Ile Val Glu Arg His
        595                 600                 605
Val Leu Arg Ala His Thr Phe Ser Ala Gln Ser Gly Tyr Arg Val Pro
    610                 615                 620
Gly Pro Gln Pro Gly His Lys His Ser Leu Ser Ser Gly Gly Phe Ser
625                 630                 635                 640
Pro Val Ala Gly Val Gly Ala Gln Asp Gly Asp Tyr Gln Arg Pro His
                645                 650                 655
Ser Ala Gln Pro Ala Asp Arg Gly Tyr Asp Arg Pro Lys Ala Val Ser
            660                 665                 670
Ala Leu Ala Thr Glu Ser Gly His Pro Asp Ser Gln Lys Pro Pro Thr
        675                 680                 685
His Pro Gly Thr Ser Asp Ser Tyr Ser Ala Pro Arg Asp Cys Leu Thr
    690                 695                 700
Pro Leu Asn Gln Thr Ala Met Thr Ala Leu Leu
705                 710                 715
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<213> Mus musculus

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<221> CDS
<222> (129)...(1640)

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aggcgggcag cggcagtgta gagccgggcc gggaggccga tcctgcgggt ctggagtccg       120
gcgggacc atg ggg acc ggg gct ggt ggg ccg agt gtc ctg gcg ctg ctg       170
         Met Gly Thr Gly Ala Gly Gly Pro Ser Val Leu Ala Leu Leu
          1               5                   10
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```
ttc gcc gtg tgt gct ccg ctc cgg ttg cag gcg gag gag ctg ggt gat      218
Phe Ala Val Cys Ala Pro Leu Arg Leu Gln Ala Glu Glu Leu Gly Asp
 15                  20                  25                  30


ggc tgt ggg cac ata gtg acc tct cag gac agt ggc aca atg aca tct      266
Gly Cys Gly His Ile Val Thr Ser Gln Asp Ser Gly Thr Met Thr Ser
                 35                  40                  45


aag aat tat cca ggg act tac ccc aat tac act gtg tgt gaa aag atc      314
Lys Asn Tyr Pro Gly Thr Tyr Pro Asn Tyr Thr Val Cys Glu Lys Ile
                 50                  55                  60


atc aca gtc cca aag ggg aag aga ctt att ctg agg ttg gga gat ttg      362
Ile Thr Val Pro Lys Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu
                 65                  70                  75


aac att gag tcc aag acc tgc gct tct gac tat ctc ctc ttc agc agt      410
Asn Ile Glu Ser Lys Thr Cys Ala Ser Asp Tyr Leu Leu Phe Ser Ser
             80                  85                  90


gca aca gat cag tat ggt cca tat tgt ggg agt tgg gct gtt ccc aaa      458
Ala Thr Asp Gln Tyr Gly Pro Tyr Cys Gly Ser Trp Ala Val Pro Lys
 95                 100                 105                 110


gaa ctc cgg ctg aac tca aac gaa gtg act gtc ctc ttc aag agt gga      506
Glu Leu Arg Leu Asn Ser Asn Glu Val Thr Val Leu Phe Lys Ser Gly
                115                 120                 125


tct cac att tct ggc cgg ggc ttt ctg ctg acc tac gcc agc agt gac      554
Ser His Ile Ser Gly Arg Gly Phe Leu Leu Thr Tyr Ala Ser Ser Asp
                130                 135                 140


cat cca gat tta ata acc tgt ttg gaa cga ggc agc cat tat ttc gag      602
His Pro Asp Leu Ile Thr Cys Leu Glu Arg Gly Ser His Tyr Phe Glu
                145                 150                 155


gaa aaa tac agc aaa ttc tgc cca gct ggc tgt aga gac ata gca gga      650
Glu Lys Tyr Ser Lys Phe Cys Pro Ala Gly Cys Arg Asp Ile Ala Gly
                160                 165                 170


gat att tct ggg aat aca aaa gat ggt tac aga gat acc tct tta ttg      698
Asp Ile Ser Gly Asn Thr Lys Asp Gly Tyr Arg Asp Thr Ser Leu Leu
                175                 180                 185                 190
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tgc aaa gct gcc atc cac gca ggg atc atc aca gat gaa cta ggt ggc   746
Cys Lys Ala Ala Ile His Ala Gly Ile Ile Thr Asp Glu Leu Gly Gly
             195   200   205

cac atc aac ttg ctt cag agc aaa ggg ata agt cac tat gaa gga ctc   794
His Ile Asn Leu Leu Gln Ser Lys Gly Ile Ser His Tyr Glu Gly Leu
             210   215   220

ctg gcc aat ggc gtg ctc tcc cgg cat ggt tct ttg tcg gaa aag cga   842
Leu Ala Asn Gly Val Leu Ser Arg His Gly Ser Leu Ser Glu Lys Arg
             225   230   235

ttt ctt ttt aca acc cca gga atg aat att aca act gtg gcg att cca   890
Phe Leu Phe Thr Thr Pro Gly Met Asn Ile Thr Thr Val Ala Ile Pro
     240   245   250

tca gtg atc ttc atc gcc ctc ctt ctg act gga atg ggg atc ttt gca   938
Ser Val Ile Phe Ile Ala Leu Leu Leu Thr Gly Met Gly Ile Phe Ala
255   260   265   270

atc tgt aga aag agg aaa aag aaa gga aat cca tat gtg tca gct gac   986
Ile Cys Arg Lys Arg Lys Lys Lys Gly Asn Pro Tyr Val Ser Ala Asp
             275   280   285

gct cag aaa aca ggc tgt tgg aag cag att aaa tat ccc ttt gcc agg   1034
Ala Gln Lys Thr Gly Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg
             290   295   300

cat cag tcg acg gaa ttt acc atc agc tat gac aat gaa aaa gag atg   1082
His Gln Ser Thr Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu Met
             305.   310   315

aca caa aag ttg gat ctc atc act agt gat atg gca gat tat cag cag   1130
Thr Gln Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr Gln Gln
             320   325   330

cct ctc atg att ggc aca ggc aca gtc gcg aga aag ggc tct acc ttc   1178
Pro Leu Met Ile Gly Thr Gly Thr Val Ala Arg Lys Gly Ser Thr Phe
335   340   345   350

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cga ccc atg gac aca gac act gag gag gtc aga gtg aac act gag gcc    1226
Arg Pro Met Asp Thr Asp Thr Glu Glu Val Arg Val Asn Thr Glu Ala
            355             360             365


agc ggc cac tat gac tgt cct cac cgc ccg ggc cgc cat gag tac gca    1274
Ser Gly His Tyr Asp Cys Pro His Arg Pro Gly Arg His Glu Tyr Ala
            370             375             380


ctg cct ttg acg cac tca gaa cct gag tat gcc aca cct atc gtg gag    1322
Leu Pro Leu Thr His Ser Glu Pro Glu Tyr Ala Thr Pro Ile Val Glu
            385             390             395


cgg cac ctg ctg cga gct cac acc ttc tcc aca cag agc ggc tac cga    1370
Arg His Leu Leu Arg Ala His Thr Phe Ser Thr Gln Ser Gly Tyr Arg
        400             405             410


gtc cct ggg ccc agg ccc act cac aaa cac tcc cat tcc tct gga ggc    1418
Val Pro Gly Pro Arg Pro Thr His Lys His Ser His Ser Ser Gly Gly
415             420             425             430


ttt cct cct gct aca gga gcc acc cag gtt gaa agc tat cag agg cca    1466
Phe Pro Pro Ala Thr Gly Ala Thr Gln Val Glu Ser Tyr Gln Arg Pro
            435             440             445


gca agc ccc aag cct gtg ggt ggt ggc tat gac aag cct gct gct agc    1514
Ala Ser Pro Lys Pro Val Gly Gly Gly Tyr Asp Lys Pro Ala Ala Ser
            450             455             460


agc ttc ttg gac agc aga gac cca gcc tct cag tca cag atg act tcc    1562
Ser Phe Leu Asp Ser Arg Asp Pro Ala Ser Gln Ser Gln Met Thr Ser
            465             470             475


ggg gga gat gat ggt tat tcg gca ccc aga aac ggt ctt gcg ccc ctc    1610
Gly Gly Asp Asp Gly Tyr Ser Ala Pro Arg Asn Gly Leu Ala Pro Leu
            480             485             490


aac cag acg gcc atg act gct ctt ttg tga acccaatgtg aaagaaacct      1660
Asn Gln Thr Ala Met Thr Ala Leu Leu  *
495                 500


gctgtggtac tgagcgcgca ccgctgcgag tcactggaag aaatgtgcaa gcgtgcatgt   1720
gtgactcttc aggatcctag agacgacctc acttactgtt tacagaactg tgcagctggt   1780
ttagttccaa cccttcctgc agagccagtt ggtttctgtt gtgctagaac aagggggactt   1840
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ttctcatttg tcttaactgt gatgctgtgc tgtaaaatgt gcaatttgta cagttatatt    1900
taacacgaat taacattacg aagtttgcgg tgtttgtttt ctacacaggg cttaaggaga    1960
aaacacggga tttgtatagc ggtagcctgt gtttctcagt gtatttgatt atctgacgct    2020
gtaagcagca ggtctgttta aaaacctcgt tggttgttgt ggctctttcc tttttgataa    2080
agtaaaagca tttttaccgc tttgtctcct ggaagaaatg aaattacttg aaacatgtaa    2140
agcactccag gataggtgat tgctagcaat ggtggcccat ttatgcaagc aaacatctga    2200
ctttagcagc tgcagcctgc tttcttagac tttccttgag aggtagggca gcctagtgtc    2260
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ttcttacaac tttctccaga gataatgcat gtgggtgact tccactatcc ctggaaaaca    2560
aatgtcgggt catatggctt cgcgcatgcg cagaagcaga gcttttctag tggcgcgcta    2620
gtaactgtcc tggtgatgta aaaagcagtt ttcttttttcc cctgcatacg tgcttatact    2680
catagagtag cccatgtctc ggctgtacct catgttttgt gttgtttttc cctgagtttt    2740
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<210> 4
<211> 503
<212> PRT
<213> Mus musculus

<400> 4

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1               5                   10                  15
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            20                  25                  30
Gly His Ile Val Thr Ser Gln Asp Ser Gly Thr Met Thr Ser Lys Asn
        35                  40                  45
Tyr Pro Gly Thr Tyr Pro Asn Tyr Thr Val Cys Glu Lys Ile Ile Thr
    50                  55                  60
Val Pro Lys Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu Asn Ile
65                  70                  75                  80
Glu Ser Lys Thr Cys Ala Ser Asp Tyr Leu Leu Phe Ser Ser Ala Thr
                85                  90                  95
Asp Gln Tyr Gly Pro Tyr Cys Gly Ser Trp Ala Val Pro Lys Glu Leu
            100                 105                 110
Arg Leu Asn Ser Asn Glu Val Thr Val Leu Phe Lys Ser Gly Ser His
        115                 120                 125
Ile Ser Gly Arg Gly Phe Leu Leu Thr Tyr Ala Ser Ser Asp His Pro
    130                 135                 140
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Asp Leu Ile Thr Cys Leu Glu Arg Gly Ser His Tyr Phe Glu Glu Lys
145                 150                 155                 160
Tyr Ser Lys Phe Cys Pro Ala Gly Cys Arg Asp Ile Ala Gly Asp Ile
                165                 170                 175
Ser Gly Asn Thr Lys Asp Gly Tyr Arg Asp Thr Ser Leu Leu Cys Lys
            180                 185                 190
Ala Ala Ile His Ala Gly Ile Ile Thr Asp Glu Leu Gly Gly His Ile
        195                 200                 205
Asn Leu Leu Gln Ser Lys Gly Ile Ser His Tyr Glu Gly Leu Leu Ala
    210                 215                 220
Asn Gly Val Leu Ser Arg His Gly Ser Leu Ser Glu Lys Arg Phe Leu
225                 230                 235                 240
Phe Thr Thr Pro Gly Met Asn Ile Thr Thr Val Ala Ile Pro Ser Val
                245                 250                 255
Ile Phe Ile Ala Leu Leu Leu Thr Gly Met Gly Ile Phe Ala Ile Cys
                260                 265                 270
Arg Lys Arg Lys Lys Lys Gly Asn Pro Tyr Val Ser Ala Asp Ala Gln
        275                 280                 285
Lys Thr Gly Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg His Gln
    290                 295                 300
Ser Thr Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu Met Thr Gln
305                 310                 315                 320
Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr Gln Gln Pro Leu
                325                 330                 335
Met Ile Gly Thr Gly Thr Val Ala Arg Lys Gly Ser Thr Phe Arg Pro
            340                 345                 350
Met Asp Thr Asp Thr Glu Glu Val Arg Val Asn Thr Glu Ala Ser Gly
        355                 360                 365
His Tyr Asp Cys Pro His Arg Pro Gly Arg His Glu Tyr Ala Leu Pro
    370                 375                 380
Leu Thr His Ser Glu Pro Glu Tyr Ala Thr Pro Ile Val Glu Arg His
385                 390                 395                 400
Leu Leu Arg Ala His Thr Phe Ser Thr Gln Ser Gly Tyr Arg Val Pro
                405                 410                 415
Gly Pro Arg Pro Thr His Lys His Ser His Ser Ser Gly Gly Phe Pro
            420                 425                 430
Pro Ala Thr Gly Ala Thr Gln Val Glu Ser Tyr Gln Arg Pro Ala Ser
            435                 440                 445
Pro Lys Pro Val Gly Gly Gly Tyr Asp Lys Pro Ala Ala Ser Ser Phe
    450                 455                 460
Leu Asp Ser Arg Asp Pro Ala Ser Gln Ser Gln Met Thr Ser Gly Gly
465                 470                 475                 480
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Thr Ala Met Thr Ala Leu Leu
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agagccgggc cgggaggccg atcctgcggg tctggagtcc ggcgggacc atg ggg acc   118
                                                      Met Gly Thr
                                                        1


ggg gct ggt ggg ccg agt gtc ctg gcg ctg ctg ttc gcc gtg tgt gct   166
Gly Ala Gly Gly Pro Ser Val Leu Ala Leu Leu Phe Ala Val Cys Ala
     5                  10                  15


ccg ctc cgg ttg cag gcg gag gag ctg ggt gat ggc tgt ggg cac ata   214
Pro Leu Arg Leu Gln Ala Glu Glu Leu Gly Asp Gly Cys Gly His Ile
 20                  25                  30                  35


gtg acc tct cag gac agt ggc aca atg aca tct aag aat tat cca ggg   262
Val Thr Ser Gln Asp Ser Gly Thr Met Thr Ser Lys Asn Tyr Pro Gly
                 40                  45                  50


act tac ccc aat tac act gtg tgt gaa aag atc atc aca gtc cca aag   310
Thr Tyr Pro Asn Tyr Thr Val Cys Glu Lys Ile Ile Thr Val Pro Lys
                 55                  60                  65


ggg aag aga ctt att ctg agg ttg gga gat ttg aac att gag tcc aag   358
Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu Asn Ile Glu Ser Lys
             70                  75                  80


acc tgc gct tct gac tat ctc ctc ttc agc agt gca aca gat cag tat   406
Thr Cys Ala Ser Asp Tyr Leu Leu Phe Ser Ser Ala Thr Asp Gln Tyr
         85                  90                  95
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gat tta ata acc tgt ttg gaa cga ggc agc cat tat ttc gag gaa aaa      454
Asp Leu Ile Thr Cys Leu Glu Arg Gly Ser His Tyr Phe Glu Glu Lys
100             105             110                 115

tac agc aaa ttc tgc cca gct ggc tgt aga gac ata gca gga gat att      502
Tyr Ser Lys Phe Cys Pro Ala Gly Cys Arg Asp Ile Ala Gly Asp Ile
                120             125             130

tct ggg aat aca aaa gat ggt tac aga gat acc tct tta ttg tgc aaa      550
Ser Gly Asn Thr Lys Asp Gly Tyr Arg Asp Thr Ser Leu Leu Cys Lys
            135             140             145

gct gcc atc cac gca ggg atc atc aca gat gaa cta ggt ggc cac atc      598
Ala Ala Ile His Ala Gly Ile Ile Thr Asp Glu Leu Gly Gly His Ile
            150             155             160

aac ttg ctt cag agc aaa ggg ata agt cac tat gaa gga ctc ctg gcc      646
Asn Leu Leu Gln Ser Lys Gly Ile Ser His Tyr Glu Gly Leu Leu Ala
        165             170             175

aat ggc gtg ctc tcc cgg cat ggt tct ttg tcg gaa aag cga ttt ctt      694
Asn Gly Val Leu Ser Arg His Gly Ser Leu Ser Glu Lys Arg Phe Leu
180             185             190                 195

ttt aca acc cca gga atg aat att aca act gtg gcg att cca tca gtg      742
Phe Thr Thr Pro Gly Met Asn Ile Thr Thr Val Ala Ile Pro Ser Val
                200             205                 210

atc ttc atc gcc ctc ctt ctg act gga atg ggg atc ttt gca atc tgt      790
Ile Phe Ile Ala Leu Leu Leu Thr Gly Met Gly Ile Phe Ala Ile Cys
            215             220             225

aga aag agg aaa aag aaa gga aat cca tat gtg tca gct gac gct cag      838
Arg Lys Arg Lys Lys Lys Gly Asn Pro Tyr Val Ser Ala Asp Ala Gln
            230             235             240

aaa aca ggc tgt tgg aag cag att aaa tat ccc ttt gcc agg cat cag      886
Lys Thr Gly Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg His Gln
        245             250             255
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tcg acg gaa ttt acc atc agc tat gac aat gaa aaa gag atg aca caa       934
Ser Thr Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu Met Thr Gln
260             265             270             275

aag ttg gat ctc atc act agt gat atg gca gat tat cag cag cct ctc       982
Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr Gln Gln Pro Leu
            280             285             290

atg att ggc aca ggc aca gtc gcg aga aag ggc tct acc ttc cga ccc      1030
Met Ile Gly Thr Gly Thr Val Ala Arg Lys Gly Ser Thr Phe Arg Pro
            295             300             305

atg gac aca gac act gag gag gtc aga gtg aac act gag gcc agc ggc      1078
Met Asp Thr Asp Thr Glu Glu Val Arg Val Asn Thr Glu Ala Ser Gly
            310             315             320

cac tat gac tgt cct cac cgc ccg ggc cgc cat gag tac gca ctg cct      1126
His Tyr Asp Cys Pro His Arg Pro Gly Arg His Glu Tyr Ala Leu Pro
            325             330             335

ttg acg cac tca gaa cct gag tat gcc aca cct atc gtg gag cgg cac      1174
Leu Thr His Ser Glu Pro Glu Tyr Ala Thr Pro Ile Val Glu Arg His
340             345             350             355

ctg ctg cga gct cac acc ttc tcc aca cag agc ggc tac cga gtc cct      1222
Leu Leu Arg Ala His Thr Phe Ser Thr Gln Ser Gly Tyr Arg Val Pro
            360             365             370

ggg ccc agg ccc act cac aaa cac tcc cat tcc tct gga ggc ttt cct      1270
Gly Pro Arg Pro Thr His Lys His Ser His Ser Ser Gly Gly Phe Pro
            375             380             385

cct gct aca gga gcc acc cag gtt gaa agc tat cag agg cca gca agc      1318
Pro Ala Thr Gly Ala Thr Gln Val Glu Ser Tyr Gln Arg Pro Ala Ser
            390             395             400

ccc aag cct gtg ggt ggt ggc tat gac aag cct gct gct agc agc ttc      1366
Pro Lys Pro Val Gly Gly Gly Tyr Asp Lys Pro Ala Ala Ser Ser Phe
            405             410             415

ttg gac agc aga gac cca gcc tct cag tca cag atg act tcc ggg gga      1414
Leu Asp Ser Arg Asp Pro Ala Ser Gln Ser Gln Met Thr Ser Gly Gly
420             425             430             435
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gat gat ggt tat tcg gca ccc aga aac ggt ctt gcg ccc ctc aac cag       1462
Asp Asp Gly Tyr Ser Ala Pro Arg Asn Gly Leu Ala Pro Leu Asn Gln
            440                 445                 450


acg gcc atg act gct ctt ttg tga acccaatgtg aaagaaacct gctgtggtac       1516
Thr Ala Met Thr Ala Leu Leu  *
            455


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aggatcctag agacgacctc acttactgtt tacagaactg tgcagctggt ttagttccaa     1636
cccttcctgc agagccagtt ggtttctgtt gtgctagaac aaggggactt ttctcatttg     1696
tcttaactgt gatgctgtgc tgtaaaatgt gcaatttgta cagttatatt taacacgaat     1756
taacattacg aagtttgcgg tgtttgtttt ctacacaggg cttaaggaga aaacacggga     1816
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ggtctgttta aaaacctcgt tggttgttgt ggctctttcc tttttgataa agtaaaagca     1936
tttttaccgc tttgtctcct ggaagaaatg aaattacttg aaacatgtaa agcactccag     1996
gataggtgat tgctagcaat ggtggcccat ttatgcaagc aaacatctga ctttagcagc     2056
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cgtggatccc agctgcatcc tgagggacca ccttctctaa ggaaagggct tagcctactg     2176
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Gly His Ile Val Thr Ser Gln Asp Ser Gly Thr Met Thr Ser Lys Asn
  35   40   45

Tyr Pro Gly Thr Tyr Pro Asn Tyr Thr Val Cys Glu Lys Ile Ile Thr
  50   55   60

Val Pro Lys Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu Asn Ile
65   70   75   80

Glu Ser Lys Thr Cys Ala Ser Asp Tyr Leu Leu Phe Ser Ser Ala Thr
    85   90   95

Asp Gln Tyr Asp Leu Ile Thr Cys Leu Glu Arg Gly Ser His Tyr Phe
    100   105   110

Glu Glu Lys Tyr Ser Lys Phe Cys Pro Ala Gly Cys Arg Asp Ile Ala
    115   120   125

Gly Asp Ile Ser Gly Asn Thr Lys Asp Gly Tyr Arg Asp Thr Ser Leu
    130   135   140

Leu Cys Lys Ala Ala Ile His Ala Gly Ile Ile Thr Asp Glu Leu Gly
145   150   155   160

Gly His Ile Asn Leu Leu Gln Ser Lys Gly Ile Ser His Tyr Glu Gly
    165   170   175

Leu Leu Ala Asn Gly Val Leu Ser Arg His Gly Ser Leu Ser Glu Lys
    180   185   190

Arg Phe Leu Phe Thr Thr Pro Gly Met Asn Ile Thr Thr Val Ala Ile
    195   200   205

Pro Ser Val Ile Phe Ile Ala Leu Leu Leu Thr Gly Met Gly Ile Phe
  210   215   220

Ala Ile Cys Arg Lys Arg Lys Lys Lys Gly Asn Pro Tyr Val Ser Ala
225   230   235   240

Asp Ala Gln Lys Thr Gly Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala
    245   250   255

Arg His Gln Ser Thr Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu
    260   265   270

Met Thr Gln Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr Gln
    275   280   285

Gln Pro Leu Met Ile Gly Thr Gly Thr Val Ala Arg Lys Gly Ser Thr
  290   295   300

Phe Arg Pro Met Asp Thr Asp Thr Glu Glu Val Arg Val Asn Thr Glu
305   310   315   320

Ala Ser Gly His Tyr Asp Cys Pro His Arg Pro Gly Arg His Glu Tyr
    325   330   335

Ala Leu Pro Leu Thr His Ser Glu Pro Glu Tyr Ala Thr Pro Ile Val
    340   345   350

Glu Arg His Leu Leu Arg Ala His Thr Phe Ser Thr Gln Ser Gly Tyr
  355   360   365

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Arg Val Pro Gly Pro Arg Pro Thr His Lys His Ser His Ser Ser Gly
    370             375             380
Gly Phe Pro Pro Ala Thr Gly Ala Thr Gln Val Glu Ser Tyr Gln Arg
385             390             395             400
Pro Ala Ser Pro Lys Pro Val Gly Gly Gly Tyr Asp Lys Pro Ala Ala
            405             410             415
Ser Ser Phe Leu Asp Ser Arg Asp Pro Ala Ser Gln Ser Gln Met.Thr
            420             425             430
Ser Gly Gly Asp Asp Gly Tyr Ser Ala Pro Arg Asn Gly Leu Ala Pro
        435             440             445
Leu Asn Gln Thr Ala Met Thr Ala Leu Leu
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            20   25   30
Xaa Xaa Cys Xaa Xaa Xaa Xaa
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Xaa Xaa Xaa Gly
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acntayccna aycayacngt ntgygaraar acnathacng tnccnaargg naarmgnytn   240
athytnmgny tnggngayyt ngayathgar wsncaracnt gygcnwsnga ytayytnytn   300
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gtngcnggng ayathwsngg naayatggtn gayggntaym gngayacnws nytnytntgy    600
aargcngcna thcaygcngg nathathgcn gaygarytng gnggncarat hwsngtnytn    660
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wsnggngayw snwsnaayaa ycayaarccn mgngartggy tngarathga yytnggngar    960
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carmgnathg cnytnaargt ngarytnath ggntgycara thacncargg naaygaywsn   1260
ytngtntggm gnaaracnws ncarwsnacn wsngtnwsna cnaaraarga rgaygaracn   1320
athacnmgnc cnathccnws ngargaracn wsnacnggna thaayathac nacngtngcn   1380
athccnytng tnytnytngt ngtnytngtn ttygcnggna tgggnathtt ygcngcntty   1440
mgnaaraara araaraargg nwsnccntay ggnwsngcng argcncaraa racngaytgy   1500
tggaarcara thaartaycc nttygcnmgn caycarwsng cngarttyac nathwsntay   1560
gayaaygara argaratgac ncaraarytn gayytnatha cnwsngayat ggcngaytay   1620
carcarccny tnatgathgg nacnggnacn gtnacnmgna arggnwsnac nttymgnccn   1680
atggayacng aygcngarga rgcnggngtn wsnacngayg cnggnggnca ytaygaytgy   1740
ccncarmgng cnggnmgnca ygartaygcn ytnccnytng cnccnccnga rccngartay   1800
gcnacnccna thgtngarmg ncaygtnytn mgngcncaya cnttywsngc ncarwsnggn   1860
taymgngtnc cnggnccnca rccnggncay aarcaywsny tnwsnwsngg nggnttywsn   1920
ccngtngcng gngtnggngc ncargayggn gaytaycarm gnccncayws ngcncarccn   1980
gcngaymgng gntaygaymg nccnaargcn gtnwsngcny tngcnacnga rwsnggncay   2040
ccngaywsnc araarccncc nacncayccn ggnacnwsng aywsntayws ngcnccnmgn   2100
gaytgyytna cnccnytnaa ycaracngcn atgacngcny tnytn               2145
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<210> 13
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate nucleotide sequence

<221> misc_feature
<222> (1)...(1509)
<223> n = A,T,C or G

<400> 13

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ytnmgnytnc argcngarga rytnggngay ggntgyggnc ayathgtnac nwsncargay   120
wsnggnacna tgacnwsnaa raaytayccn ggnacntayc cnaaytayac ngtntgygar   180
aarathatha cngtnccnaa rggnaarmgn ytnathytnm gnytnggnga yytnaayath   240
garwsnaara cntgygcnws ngaytayytn ytnttywsnw sngcnacnga ycartayggn   300
ccntaytgyg gnwsntgggc ngtnccnaar garytnmgny tnaaywsnaa ygargtnacn   360
gtnytnttya arwsnggnws ncayathwsn ggnmgnggnt tyytnytnac ntaygcnwsn   420
wsngaycayc cngayytnat hacntgyytn garmgnggnw sncaytaytt ygargaraar   480
taywsnaart tytgyccngc nggntgymgn gayathgcng gngayathws nggnaayacn   540
aargayggnt aymgngayac nwsnytnytn tgyaargcng cnathcaygc nggnathath   600
acngaygary tnggnggnca yathaayytn ytncarwsna arggnathws ncaytaygar   660
ggnytnytng cnaayggngt nytnwsnmgn cayggnwsny tnwsngaraa rmgnttyytn   720
ttyacnacnc cnggnatgaa yathacnacn gtngcnathc cnwsngtnat httyathgcn   780
ytnytnytna cnggnatggg nathtttygcn athtgymgna armgnaaraa raarggnaay   840
ccntaygtnw sngcngaygc ncaraaracn ggntgytgga arcarathaa rtayccntty   900
gcnmgncayc arwsnacnga rttyacnath wsntaygaya aygaraarga ratgacncar   960
aarytngayy tnathacnws ngayatggcn gaytaycarc arccnytnat gathggnacn  1020
ggnacngtng cnmgnaargg nwsnacntty mgnccnatgg ayacngayac ngargargtn  1080
mgngtnaaya cngargcnws nggncaytay gaytgyccnc aymgnccngg nmgncaygar  1140
taygcnytnc cnytnacnca ywsngarccn gartaygcna cnccnathgt ngarmgncay  1200
ytnytnmgng cncayacntt ywsnacncar wsnggntaym gngtnccngg nccnmgnccn  1260
acncayaarc aywsncayws nwsnggnggn ttyccnccng cnacnggngc nacncargtn  1320
garwsntayc armgnccngc nwsnccnaar ccngtnggng gnggntayga yaarccngcn  1380
gcnwsnwsnt tyytngayws nmgngayccn gcnwsncarw sncaratgac nwsnggnggn  1440
gaygayggnt aywsngcncc nmgnaayggn ytngcnccny tnaaycarac ngcnatgacn  1500
gcnytnytn                                                          1509
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<210> 14
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate nucleotide sequence

<221> misc_feature
<222> (1)...(1374)
<223> n = A,T,C or G

<400> 14

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ytnmgnytnc argcngarga rytnggngay ggntgyggnc ayathgtnac nwsncargay   120
```

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wsnggnacna tgacnwsnaa raaytayccn ggnacntayc cnaaytayac ngtntgygar    180
aarathatha cngtnccnaa rggnaarmgn ytnathytnm gnytnggnga yytnaayath    240
garwsnaara cntgygcnws ngaytayytn ytnttywsnw sngcnacnga ycartaygay    300
ytnathacnt gyytngarmg nggnwsncay tayttygarg araartayws naarttytgy    360
ccngcnggnt gymgngayat hgcnggngay athwsnggna ayacnaarga yggntaymgn    420
gayacnwsny tnytntgyaa rgcngcnath caygcnggna thathacnga ygarytnggn    480
ggncayatha ayytnytnca rwsnaarggn athwsncayt aygarggnyt nytngcnaay    540
ggngtnytnw snmgncaygg nwsnytnwsn garaarmgnt tyytnttyac nacnccnggn    600
atgaayatha cnacngtngc nathccnwsn gtnathttya thgcnytnyt nytnacnggn    660
atgggnatht tygcnathtg ymgnaarmgn aaraaraarg gnaayccnta ygtnwsngcn    720
gaygcncara aracnggntg ytggaarcar athaartayc cnttygcnmg ncaycarwsn    780
acngarttya cnathwsnta ygayaaygar aargaratga cncaraaryt ngayytnath    840
acnwsngaya tggcngayta ycarcarccn ytnatgathg gnacnggnac ngtngcnmgn    900
aarggnwsna cnttymgncc natggayacn gayacngarg argtnmgngt naayacngar    960
gcnwsnggnc aytaygaytg yccncaymgn ccnggnmgnc aygartaygc nytnccnytn   1020
acncaywsng arccngarta ygcnacnccn athgtngarm gncayytnyt nmgngcncay   1080
acnttywsna cncarwsngg ntaymgngtn ccnggnccnm gnccnacnca yaarcaywsn   1140
caywsnwsng gnggnttycc nccngcnacn ggngcnacnc argtngarws ntaycarmgn   1200
ccngcnwsnc cnaarccngt nggnggnggn taygayaarc cngcngcnws nwsnttyytn   1260
gaywsnmgng ayccngcnws ncarwsncar atgacnwsng gnggngayga yggntaywsn   1320
gcnccnmgna ayggnytngc nccnytnaay caracngcna tgacngcnyt nytn         1374
```

<210> 15
<211> 1001
<212> DNA
<213> Homo sapiens

<400> 15

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ccgaggacca agttaaacat cctttaggtt atttagctgc acgtcctggc ccctactctg     60
tacactagct tctacatctg gccgtgtacc cacctgttca ctgtgctcca gctacctggc    120
cctttcctcc ttcagcttct ttgcacaact tgtctgtttt ggctcctgct ttaatctcag    180
ctttgatgcc acttaggcct ttcctagctg attcccgccc tcacccctgt tacccgccat    240
ctaattacag ctctctaaat gtgcttcaac agcacctttc atgtcactga ttgcaatttg    300
cattgaatac ttgcctgatt atttttgtct gcaagtgcca catgggttta gccctgctcc    360
tgacaagcac actgctgaac tgagtaactt ttgaatgaat gaatgaatga gtgaataaat    420
cagtgaaggt cctacttggc actgtcatca tcctatcatc aaaatatttc gagtccctcg    480
gtgttgctat ccctggcatg cccatccccg cgggctggca aaaccctgga gggggcagcc    540
tcccaaggca ccgccgcggg ctcagcccat ctaggaatga ctcccgcacc acgcggcgag    600
gggcgggtcc ggcggcgagg tgtcctgctg cctagcaggt tcacgtgtac tggtgcaggt    660
ggggaggaag gcaaggaagg agcgcagcag ggcgcgccag atacgtggag gggagcgcgg    720
gcggcgcctc gctcgcctcc ggcttcgccg tcggtcactg cctgggaacg cgacttcctc    780
ctctaggggc cgacgtgcgg ggcggggcgg ggccgggcgg gagacgcccc cgcagggctg    840
ggctgaaagc cgccccaatg ggattcggtg cggggcagcg actgcgcccc gtcccggcgc    900
```

cgcgctcgtc cgcagaggag gcggcccggc ccgggcagct gcggctcggg atccgtcgag   960
gggaggccga gcttgccaag ctggcgccca gcggggtcat g   1001

        <210> 16
        <211> 25
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> oligonucleotide primer ZC28,497

        <400> 16
ggcacatagt gacctctcag gacag   25

        <210> 17
        <211> 25
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> oligonucleotide primer ZC28,498

        <400> 17
tcaatgttca aatctcccaa cctca   25

        <210> 18
        <211> 20
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> oligonucleotide primer ZC28,499

        <400> 18
ggtcgctgct cgcataggtc   20

        <210> 19
        <211> 24
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> oligonucleotide primer ZC28,500

<400> 19
ctgattctga ggttgggaga tttg   24